Claim 8. (Amended) The method of Claim [1,] 2, [3, 4,] 5, 6, or 7, wherein the targets are base sequence variations selected from the group consisting of single nucleotide polymorphism, multibase deletion, multibase insertion, microsatellite repeats, di-nucleotide repeats, tri-nucleotide repeats, sequence rearrangements, and chimeric sequence.

REMARKS

Claim 1 is proposed to claim an aspect of the present invention not presented in the original claims. Claim 8 is amended in view of the limitations in Claim 1.

Support for Claim 1 is found particularly in Figure 1 and on Page 11, lines 23-30/Page 12, lines 1-30/Page 13, lines 1-19.

Entry of this amendment is respectfully requested.

Respectfully submitted,

Date: 6 Nov. 2002

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ATTACHMENT A

CLEAN VERSION OF EACH REPLACEMENT CLAIMS

Claim 1. (Amended) A method for characterizing a genetic profile of a selected chromosome pair, comprising:

forming multiple luminescent hybridization probes to hybridize to a wild-type and a mutant polymorphism at a first polymorphic target site and to a wild-type and a mutant polymorphism at a second polymorphic target site, where the probes for the wild-type polymorphic sites have at least one recognizable luminescent characteristic and the probes for the mutant polymorphic sites have at least a second recognizable luminescent characteristic and where the first and second polymorphic sites are located on the selected chromosome and are linked to a selected genetic characteristic;

forming single stranded DNA at least along segments of DNA forming the chromosome, where the single stranded DNA segments contain the first and second polymorphic sites;

forming probe pairs from the luminescent probes, where each probe pair contains a probe specific to the first polymorphic site and a probe specific to the second polymorphic site;

specifically hybridizing each probe pair in separate solutions of the single stranded DNA and determining the presence or absence of each luminescent hybridization probe in each segment of DNA in each solution to obtain a set of outputs; and

analyzing the set of outputs from the hybridized probes to determine the complete haplotype that characterizes the genetic profile of the selected chromosome pair.

Claim 8. (Amended) The method of Claim 2, 5, 6, or 7, wherein the targets are base sequence variations selected from the group consisting of single nucleotide polymorphism, multibase deletion, multibase insertion, microsatellite repeats, di-nucleotide repeats, tri-nucleotide repeats, sequence rearrangements, and chimeric sequence.